

**results of BLAST**

BLASTN 2.2.13 [Nov-27-2005]

RID: 1137952029-19170-147766514851.BLASTQ4

Database: env_nt

1,047,779 sequences; 1,063,283,128 total letters

Query=

Length=967

No significant similarity found. For reasons why, [click here](#).

Database: environmental samples

Posted date: Jan 20, 2006 5:47 PM

Number of letters in database: 1,063,283,128

Number of sequences in database: 1,047,779

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 1047779

Number of Hits to DB: 325625

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Number of extra gapped extensions for HSPs above 10: 0

Length of query: 967

Length of database: 1063283128

Length adjustment: 29

Effective length of query: 938

Effective length of database: 1063283128

Effective search space: 997359574064

Effective search space used: 968857889706

A: 0

X1: 13 (25.0 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 13 (25.1 bits)

S2: 20 (38.1 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
 RID: 1137951578-11832-159027920999.BLASTQ4

Database: Whole-Genome-Shotgun Sequences
 11,094,912 sequences; 59,568,598,518 total letters

Query=
 Length=967

No significant similarity found. For reasons why, [click here](#).

Database: Whole-Genome-Shotgun Sequences
 Posted date: Jan 20, 2006 2:58 AM
 Number of letters in database: -560,943,622
 Number of sequences in database: 11,094,912

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 11094912
 Number of Hits to DB: 10749058
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Number of extra gapped extensions for HSPs above 10: 0
 Length of query: 967
 Length of database: 59568598518
 Length adjustment: 34
 Effective length of query: 933
 Effective length of database: 59568598518
 Effective search space: 55577502417294
 Effective search space used: 55225549618830
 A: 0
 X1: 15 (28.8 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 15 (28.8 bits)
 S2: 23 (43.6 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137951413-29994-209910067433.BLASTQ4

Database: dbsts
880,418 sequences; 495,360,267 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: Database of GenBank+EMBL+DDBJ sequences from STS Divisions
Posted date: Jan 20, 2006 5:47 PM
Number of letters in database: 495,360,267
Number of sequences in database: 880,418

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 880418
Number of Hits to DB: 175557
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 495360267
Length adjustment: 28
Effective length of query: 939
Effective length of database: 495360267
Effective search space: 465143290713
Effective search space used: 441995340657
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 19 (36.2 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
 RID: 1137949086-24714-96665004932.BLASTQ4

Database: NCBI Transcript Reference Sequences
 643,718 sequences; 1,100,743,594 total letters

Query=
 Length=967

No significant similarity found. For reasons why, [click here](#).

Database: NCBI Transcript Reference Sequences
 Posted date: Jan 20, 2006 6:43 AM
 Number of letters in database: 1,100,743,594
 Number of sequences in database: 643,718

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 643718
 Number of Hits to DB: 364492
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Number of extra gapped extensions for HSPs above 10: 0
 Length of query: 967
 Length of database: 1100743594
 Length adjustment: 29
 Effective length of query: 938
 Effective length of database: 1100743594
 Effective search space: 1032497491172
 Effective search space used: 1014987074136
 A: 0
 X1: 14 (26.9 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 14 (27.0 bits)
 S2: 20 (38.1 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137950725-19945-98901092870.BLASTQ4

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions
32,883,501 sequences; 18,149,494,461 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions
Posted date: Jan 19, 2006 7:01 PM
Number of letters in database: 969,625,277
Number of sequences in database: 32,883,501

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 32883501
Number of Hits to DB: 3223832
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 18149494461
Length adjustment: 32
Effective length of query: 935
Effective length of database: 18149494461
Effective search space: 16969777321035
Effective search space used: 15985902971115
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 22 (41.7 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137950842-32735-135719625949.BLASTQ4

Database: GenBank Mouse EST entries
4,689,058 sequences; 2,178,201,793 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: GenBank Mouse EST entries
Posted date: Jan 19, 2006 7:01 PM
Number of letters in database: -2,116,765,499
Number of sequences in database: 4,689,058
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 4689058
Number of Hits to DB: 1414585
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 2178201793
Length adjustment: 30
Effective length of query: 937
Effective length of database: 2178201793
Effective search space: 2040975080041
Effective search space used: 1909165659661
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 20 (38.1 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137950767-20723-57724415792.BLASTQ4

Database: GenBank Human EST entries
7,596,952 sequences; 4,054,674,759 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: GenBank Human EST entries
Posted date: Jan 19, 2006 7:01 PM
Number of letters in database: -240,292,533
Number of sequences in database: 7,596,952

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 7596952
Number of Hits to DB: 3027239
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 4054674759
Length adjustment: 30
Effective length of query: 937
Effective length of database: 4054674759
Effective search space: 3799230249183
Effective search space used: 3585679928463
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 21 (39.9 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137950880-22256-80575218585.BLASTQ1

Database: GenBank non-mouse and non-human EST entries
20,597,491 sequences; 11,916,617,909 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: GenBank non-mouse and non-human EST entries
Posted date: Jan 19, 2006 7:01 PM
Number of letters in database: -968,283,975
Number of sequences in database: 20,597,491
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 20597491
Number of Hits to DB: 1057613
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 11916617909
Length adjustment: 32
Effective length of query: 935
Effective length of database: 11916617909
Effective search space: 11142037744915
Effective search space used: 10525760814195
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 22 (41.7 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
 RID: 1137950919-1191-16096741589.BLASTQ4

Database: Genome Survey Sequence, includes single-pass genomic data,
 exon-trapped sequences, and Alu PCR sequences.

13,851,539 sequences; 8,693,784,561 total letters

Query=
 Length=967

No significant similarity found. For reasons why, [click here](#).

Database: Genome Survey Sequence, includes single-pass genomic data, exon-trapped
 sequences, and Alu PCR sequences.

Posted date: Jan 19, 2006 6:47 PM

Number of letters in database: 103,849,969

Number of sequences in database: 13,851,539

Lambda	K	H
1.33	0.621	1.12

Gapped		
Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 13851539

Number of Hits to DB: 1359732

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Number of extra gapped extensions for HSPs above 10: 0

Length of query: 967

Length of database: 8693784561

Length adjustment: 31

Effective length of query: 936

Effective length of database: 8693784561

Effective search space: 8137382349096

Effective search space used: 7735466093472

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 12 (23.3 bits)

S2: 21 (39.9 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
 RID: 1137951011-2946-124529634406.BLASTQ4

Database: Unfinished High Throughput Genomic Sequences; Sequences:
 phases 0,1 and 2
 80,682 sequences; 13,078,902,990 total letters

Query=
 Length=967

No significant similarity found. For reasons why, [click here](#).

Database: Unfinished High Throughput Genomic Sequences; Sequences: phases 0,1 and 2

Posted date: Jan 20, 2006 6:06 AM
 Number of letters in database: 194,001,102
 Number of sequences in database: 80,682
 Lambda K H
 1.33 0.621 1.12
 Gapped
 Lambda K H
 1.33 0.621 1.12
 Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 0, Extension: 0
 Number of Sequences: 80682
 Number of Hits to DB: 2351510
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Number of extra gapped extensions for HSPs above 10: 0
 Length of query: 967
 Length of database: 13078902990
 Length adjustment: 32
 Effective length of query: 935
 Effective length of database: 13078902990
 Effective search space: 12228774295650
 Effective search space used: 12226360290210
 A: 0
 X1: 18 (34.6 bits)
 X2: 32 (59.1 bits)
 X3: 54 (99.7 bits)
 S1: 18 (34.4 bits)
 S2: 22 (41.7 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137951230-7292-44642878298.BLASTQ4

Database: PDB nucleotide database
6021 sequences; 393,392 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database: PDB nucleotide database
Posted date: Jan 20, 2006 6:43 AM
Number of letters in database: 393,392
Number of sequences in database: 6,021
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 6021
Number of Hits to DB: 702
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 393392
Length adjustment: 19
Effective length of query: 948
Effective length of database: 393392
Effective search space: 372935616
Effective search space used: 264485364
A: 0
X1: 9 (17.3 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 9 (17.7 bits)
S2: 13 (25.1 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]
RID: 1137951380-29298-143765992848.BLASTQ4

Database: alu
327 sequences; 80,506 total letters

Query=
Length=967

No significant similarity found. For reasons why, [click here](#).

Database:
Posted date: Dec 12, 2002 2:17 PM
Number of letters in database: 80,506
Number of sequences in database: 327
Lambda K H
1.33 0.621 1.12
Gapped
Lambda K H
1.33 0.621 1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 327
Number of Hits to DB: 122
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 10: 0
Length of query: 967
Length of database: 80506
Length adjustment: 18
Effective length of query: 949
Effective length of database: 80506
Effective search space: 76400194
Effective search space used: 70814380
A: 0
X1: 11 (21.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 11 (21.4 bits)
S2: 12 (23.3 bits)



results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Query:

Database: chromosome

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

1 hits found

1_10879	gi 11528013 ref NC_001563.2	82.94	985	130	37	1	967
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results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Query:

Database: month

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

2 hits found

1_7997	gi 84028432 gb DQ318019.1	83.05	985	129	37	1	967
1_7997	gi 84028434 gb DQ318020.1	82.96	986	128	38	1	967



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Query:

Database: refseq_genomic

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

1 hits found

1_25498	gi 11528013 ref NC_001563.2	82.94	985	130	37	1	967
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results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Query:

Database: pat

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

15 hits found

1_5331	gi 27647035 emb AX577796.1	98.76	970	4	7	1	967
1_5331	gi 27646162 emb AX576542.1	98.76	970	4	7	1	967
1_5331	gi 52747867 emb CQ874691.1	100.00	566	0	0	402	967
1_5331	gi 52745306 emb CQ871188.1	100.00	566	0	0	402	967
1_5331	gi 51997335 emb CQ867049.1	100.00	566	0	0	402	967
1_5331	gi 15554477 emb AX224225.1	100.00	545	0	0	423	967
1_5331	gi 52747866 emb CQ874690.1	100.00	48	0	0	920	967
1_5331	gi 44845960 emb CQ754934.1	100.00	48	0	0	920	967
1_5331	gi 44845959 emb CQ754933.1	100.00	48	0	0	920	967
1_5331	gi 44845219 emb CQ753917.1	100.00	48	0	0	920	967
1_5331	gi 44845215 emb CQ753913.1	100.00	48	0	0	920	967
1_5331	gi 44845214 emb CQ753912.1	100.00	48	0	0	920	967
1_5331	gi 27646165 emb AX576545.1	88.24	51	4	2	435	484
1_5331	gi 15554499 emb AX224249.1	100.00	29	0	0	423	451
1_5331	gi 27646166 emb AX576546.1	100.00	28	0	0	1	28



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Query:

Database: nr

Fields: query id, subject ids, % identity, alignment length, mismatches, gap opens, q

100 hits found

1_7710	gi 77980183 gb AY848696.2	98.87	970	3	7	1	967
1_7710	gi 77980181 gb AY848695.2	98.87	970	3	7	1	967
1_7710	gi 77853218 gb AY848697.2	98.87	970	3	7	1	967
1_7710	gi 66735926 gb DQ066423.1	98.87	970	3	7	1	967
1_7710	gi 75859185 gb AY842931.3	98.87	970	3	7	1	967
1_7710	gi 21929238 gb AF404756.1	98.87	970	3	7	1	967
1_7710	gi 21929232 gb AF404753.1	98.87	970	3	7	1	967
1_7710	gi 50872125 dbj AB185915.2	98.87	970	3	7	1	967
1_7710	gi 50872124 dbj AB185914.2	98.87	970	3	7	1	967
1_7710	gi 11597239 gb AF196835.2 AF196835	98.87	970	3	7	1	967
1_7710	gi 9930133 gb AF260967.1 AF260967	98.87	970	3	7	1	967
1_7710	gi 76781549 gb DQ164195.1	98.87	970	3	7	1	967
1_7710	gi 76781547 gb DQ164194.1	98.87	970	3	7	1	967
1_7710	gi 76781537 gb DQ164189.1	98.87	970	3	7	1	967
1_7710	gi 55495165 gb AY712947.1	98.76	970	4	7	1	967
1_7710	gi 77166600 gb DQ211652.1	98.76	970	4	7	1	967
1_7710	gi 21929236 gb AF404755.1	98.76	970	4	7	1	967
1_7710	gi 21929234 gb AF404754.1	98.76	970	4	7	1	967
1_7710	gi 50838784 dbj AB185917.1	98.76	970	4	7	1	967
1_7710	gi 50838782 dbj AB185916.1	98.76	970	4	7	1	967
1_7710	gi 19387527 gb AF481864.1	98.76	970	4	7	1	967
1_7710	gi 71483614 gb DQ080058.1	98.76	970	4	7	1	967
1_7710	gi 71483612 gb DQ080057.1	98.76	970	4	7	1	967
1_7710	gi 71483610 gb DQ080056.1	98.76	970	4	7	1	967
1_7710	gi 71483608 gb DQ080055.1	98.76	970	4	7	1	967
1_7710	gi 71483602 gb DQ080052.1	98.76	970	4	7	1	967
1_7710	gi 71483600 gb DQ080051.1	98.76	970	4	7	1	967
1_7710	gi 33948906 gb AY289214.1	98.76	970	4	7	1	967
1_7710	gi 76781553 gb DQ164197.1	98.76	970	4	7	1	967
1_7710	gi 76781551 gb DQ164196.1	98.76	970	4	7	1	967
1_7710	gi 76781541 gb DQ164191.1	98.76	970	4	7	1	967
1_7710	gi 76781533 gb DQ164187.1	98.76	970	4	7	1	967
1_7710	gi 76781531 gb DQ164186.1	98.76	970	4	7	1	967
1_7710	gi 55495180 gb AY712948.1	98.66	970	5	7	1	967
1_7710	gi 55495149 gb AY712946.1	98.66	970	5	7	1	967
1_7710	gi 55495130 gb AY712945.1	98.66	970	5	7	1	967
1_7710	gi 55669121 gb AY646354.1	98.66	970	5	7	1	967
1_7710	gi 26284711 gb AF533540.1	98.66	970	5	7	1	967
1_7710	gi 71483616 gb DQ080059.1	98.66	970	5	7	1	967
1_7710	gi 71483606 gb DQ080054.1	98.66	970	5	7	1	967
1_7710	gi 71483604 gb DQ080053.1	98.66	970	5	7	1	967
1_7710	gi 59876232 gb AY795965.1	98.66	970	5	7	1	967
1_7710	gi 76781569 gb DQ164205.1	98.66	970	5	7	1	967
1_7710	gi 76781567 gb DQ164204.1	98.66	970	5	7	1	967
1_7710	gi 76781565 gb DQ164203.1	98.66	970	5	7	1	967
1_7710	gi 76781563 gb DQ164202.1	98.66	970	5	7	1	967
1_7710	gi 76781559 gb DQ164200.1	98.66	970	5	7	1	967
1_7710	gi 76781557 gb DQ164199.1	98.66	970	5	7	1	967
1_7710	gi 76781555 gb DQ164198.1	98.66	970	5	7	1	967
1_7710	gi 76781545 gb DQ164193.1	98.66	970	5	7	1	967
1_7710	gi 76781543 gb DQ164192.1	98.66	970	5	7	1	967
1_7710	gi 76781535 gb DQ164188.1	98.66	970	5	7	1	967

1_7710	gi 76781571 gb DQ164206.1	98.56	970	6	7	1	967
1_7710	gi 76781561 gb DQ164201.1	98.56	970	6	7	1	967
1_7710	gi 76781539 gb DQ164190.1	98.45	970	7	7	1	967
1_7710	gi 55975602 gb AY660002.1	98.25	970	9	7	1	967
1_7710	gi 7717200 gb AF206518.2 AF206518	98.63	952	5	7	19	
1_7710	gi 71483622 gb DQ080062.1	98.83	942	3	7	29	967
1_7710	gi 71483620 gb DQ080061.1	98.83	941	3	7	30	967
1_7710	gi 71483642 gb DQ080072.1	98.72	941	4	7	30	967
1_7710	gi 71483638 gb DQ080070.1	98.51	942	6	7	29	967
1_7710	gi 71483636 gb DQ080069.1	98.51	942	6	7	29	967
1_7710	gi 71483634 gb DQ080068.1	98.51	942	6	7	29	967
1_7710	gi 71483632 gb DQ080067.1	98.51	942	6	7	29	967
1_7710	gi 71483630 gb DQ080066.1	98.51	942	6	7	29	967
1_7710	gi 71483626 gb DQ080064.1	98.51	942	6	7	29	967
1_7710	gi 71483624 gb DQ080063.1	98.51	942	6	7	29	967
1_7710	gi 71483640 gb DQ080071.1	98.41	941	7	7	30	967
1_7710	gi 71483618 gb DQ080060.1	98.41	941	7	7	30	967
1_7710	gi 71483628 gb DQ080065.1	98.50	936	6	7	35	967
1_7710	gi 6581069 gb AF202541.1 AF202541	98.71	928	4	7	43	
1_7710	gi 30349729 gb AY278441.1	97.12	971	18	9	1	967
1_7710	gi 33242576 gb AY268133.1	97.47	950	16	7	21	967
1_7710	gi 9930137 gb AF260969.1 AF260969	96.70	970	24	7	1	
1_7710	gi 21929240 gb AF404757.1	96.60	970	25	7	1	967
1_7710	gi 30349727 gb AY277252.1	96.49	970	26	7	1	967
1_7710	gi 46277828 gb AY490240.2	96.39	970	27	7	1	967
1_7710	gi 30349731 gb AY278442.1	96.39	970	27	7	1	967
1_7710	gi 51318183 gb AY603654.1	96.19	971	27	9	1	967
1_7710	gi 9930135 gb AF260968.1 AF260968	95.98	970	31	7	1	
1_7710	gi 33242574 gb AY268132.1	96.32	950	27	7	21	967
1_7710	gi 6715269 gb AF194117.1 AF194117	98.74	874	3	7	97	
1_7710	gi 12744408 gb AF317203.1 AF317203	96.38	938	26	7	33	
1_7710	gi 30230630 gb AY262283.1	96.47	934	25	7	37	967
1_7710	gi 51011375 gb AY701413.1	96.55	928	24	7	43	967
1_7710	gi 51011373 gb AY701412.1	96.23	928	27	7	43	967
1_7710	gi 17226060 gb AF375223.1 AF375223	99.87	794	1	0	174	
1_7710	gi 19421851 gb AF375044.1	99.75	794	2	0	174	967
1_7710	gi 19421847 gb AF375042.1	99.75	794	2	0	174	967
1_7710	gi 14550047 gb AF385265.1 AF385265	100.00	761	0	0	207	
1_7710	gi 14550045 gb AF385264.1 AF385264	100.00	761	0	0	207	
1_7710	gi 14550043 gb AF385263.1 AF385263	100.00	761	0	0	207	
1_7710	gi 14550041 gb AF385262.1 AF385262	100.00	761	0	0	207	
1_7710	gi 14550039 gb AF385261.1 AF385261	100.00	761	0	0	207	
1_7710	gi 14550037 gb AF385260.1 AF385260	100.00	761	0	0	207	
1_7710	gi 14550035 gb AF385259.1 AF385259	100.00	761	0	0	207	
1_7710	gi 14550033 gb AF385258.1 AF385258	100.00	761	0	0	207	
1_7710	gi 14550029 gb AF385256.1 AF385256	100.00	761	0	0	207	
1_7710	gi 14550025 gb AF385254.1 AF385254	100.00	761	0	0	207	
1_7710	gi 14550023 gb AF385253.1 AF385253	100.00	761	0	0	207	